

10/665, 715 9-0806

GenCore version 5.1.9
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 8, 2006, 08:30:26 ; Search time 0.1 Seconds
(without alignments)
7.808 Million cell updates/sec

Title: HSBTRCP
Perfect score: 3861
Sequence: 1 TGC GTTGGCTGCGGCCTGGC.....GTTTTGCCAGAAAAAAAAA 2151

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 2 seqs, 1210 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=soft -Q=y14153.gb_pr -DB=uni.pep -SUFFIX=pto
-OUT=eliz2.res -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO_XLPXY -NEG_SCORES=0
-LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : uni.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	3006	77.9	605	1	FBW1A_HUMAN	F-box/WD-repeat pr
	2	3006	77.9	605	1	FBW1A_HUMAN	F-box/WD-repeat pr
c	3	57.5	1.5	605	1	FBW1A_HUMAN	F-box/WD-repeat pr
c	4	57.5	1.5	605	1	FBW1A_HUMAN	F-box/WD-repeat pr

ALIGNMENTS

RESULT 1

FBW1A_HUMAN

ID FBW1A_HUMAN STANDARD; PRT; 605 AA.
AC Q9Y297; Q9Y213;
DT 21-FEB-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 52.
DE F-box/WD-repeat protein 1A (F-box and WD-repeats protein beta-TrCP)
DE (E3RSIkappaB) (pIkappaBalpha-E3 receptor subunit).
GN Name=BTRC; Synonyms=BTRCP, FBW1A, FBXW1A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RX MEDLINE=99075339; PubMed=9859996; DOI=10.1038/25159;
RA Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
RA Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
RT "Identification of the receptor component of the IkappaBalpha-
RT ubiquitin ligase.";
RL Nature 396:590-594(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
RC TISSUE=Lymphoid;
RX MEDLINE=98325370; PubMed=9660940; DOI=10.1016/S1097-2765(00)80056-8;
RA Margottin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V.,
RA Thomas D., Strebel K., Benarous R.;
RT "A novel human WD protein, h-beta TrCp, that interacts with HIV-1 Vpu
RT connects CD4 to the ER degradation pathway through an F-box motif.";
RL Mol. Cell 1:565-574(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
RX MEDLINE=20003060; PubMed=10531035; DOI=10.1016/S0960-9822(00)80020-2;
RA Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal M.,
RA Pagano M.;
RT "Identification of a family of human F-box proteins.";
RL Curr. Biol. 9:1177-1179(1999).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE=99145464; PubMed=9990852;
 RA Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J.,
 RA Harper J.W.;
 RT "The SCF(beta-TRCP)-ubiquitin ligase complex associates specifically
 RT with phosphorylated destruction motifs in I-kappa-B-alpha and beta-
 RT catenin and stimulates I-kappa-B-alpha ubiquitination in vitro.";
 RL Genes Dev. 13:270-283(1999).
 RN [6]
 RP INTERACTION WITH UBQLN1.
 RC TISSUE=B-cell;
 RX MEDLINE=20437281; PubMed=10983987; DOI=10.1016/S1097-2765(00)00040-X;
 RA Kleijnen M.F., Shih A.H., Zhou P., Kumar S., Soccio R.E.,
 RA Kedersha N.L., Gill G., Howley P.M.;
 RT "The hPLIC proteins may provide a link between the ubiquitination
 RT machinery and the proteasome.";
 RL Mol. Cell 6:409-419(2000).
 RN [7]
 RP INTERACTION WITH PHOSPHORYLATED CTNNB1.
 RX MEDLINE=22072105; PubMed=12077367;
 RA Sadot E., Conacci-Sorrell M., Zhurinsky J., Shnizer D., Lando Z.,
 RA Zharhary D., Kam Z., Ben-Ze'ev A., Geiger B.;
 RT "Regulation of S33/S37 phosphorylated beta-catenin in normal and
 RT transformed cells.";
 RL J. Cell Sci. 115:2771-2780(2002).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.95 ANGSTROMS) OF 175-605 IN COMPLEX WITH SKP1
 RP AND CTNNB1.
 RX MEDLINE=22706071; PubMed=12820959; DOI=10.1016/S1097-2765(03)00234-X;
 RA Wu G., Xu G., Schulman B.A., Jeffrey P.D., Harper J.W.,
 RA Pavletich N.P.;
 RT "Structure of a beta-TrCP1-Skp1-beta-catenin complex: destruction
 RT motif binding and lysine specificity of the SCF(beta-TrCP1) ubiquitin
 RT ligase.";
 RL Mol. Cell 11:1445-1456(2003).
 CC -!- FUNCTION: Substrate-recognition component of the SCF (SKP1-CUL1-F-
 CC box protein) ubiquitin ligase complex, which mediates the
 CC ubiquitination of proteins involved in cell cycle progression,
 CC signal transduction and transcription. Regulates the stability of
 CC CTNNB1 and participates in Wnt signaling.
 CC -!- PATHWAY: Ubiquitin conjugation; third step.
 CC -!- SUBUNIT: Interacts directly with SKP1 in the SCF complex.
 CC Interacts specifically with phosphorylated CTNNB1 and NFKBIA,
 CC ubiquitination substrates. Binds UBQLN1.
 CC -!- SUBCELLULAR LOCATION: Cytoplasm.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;

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CC      Name=1;
CC      IsoId=Q9Y297-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q9Y297-2; Sequence=VSP_006764;
CC      -!- SIMILARITY: Contains 1 F-box domain.
CC      -!- SIMILARITY: Contains 7 WD repeats.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AF101784; AAD08702.1; -; mRNA.
DR      EMBL; Y14153; CAA74572.1; -; mRNA.
DR      EMBL; AF129530; AAF04464.1; -; mRNA.
DR      EMBL; BC027994; AAH27994.1; -; mRNA.
DR      PDB; 1P22; X-ray; A=175-605.
DR      IntAct; Q9Y297; -.
DR      Ensembl; ENSG00000166167; Homo sapiens.
DR      HGNC; HGNC:1144; BTRC.
DR      MIM; 603482; gene.
DR      LinkHub; Q9Y297; -.
DR      GO; GO:0004840; F:ubiquitin conjugating enzyme activity; TAS.
DR      GO; GO:0007165; P:signal transduction; TAS.
DR      GO; GO:0006511; P:ubiquitin-dependent protein catabolism; TAS.
DR      InterPro; IPR001810; F-box.
DR      InterPro; IPR001680; WD40.
DR      Pfam; PF00646; F-box; 1.
DR      Pfam; PF00400; WD40; 7.
DR      PRINTS; PR00320; GPROTEINBRPT.
DR      ProDom; PD000018; WD40; 4.
DR      SMART; SM00256; FBOX; 1.
DR      SMART; SM00320; WD40; 7.
DR      PROSITE; PS50181; FBOX; 1.
DR      PROSITE; PS00678; WD_REPEATS_1; 6.
DR      PROSITE; PS50082; WD_REPEATS_2; 7.
DR      PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW      3D-structure; Alternative splicing; Ligase; Polymorphism; Repeat;
KW      Ubl conjugation pathway; WD repeat; Wnt signaling pathway.
FT      CHAIN           1           605           F-box/WD-repeat protein 1A.
FT                                     /FTId=PRO_0000050980.
FT      DOMAIN          190          228           F-box.
FT      REPEAT          301          338           WD 1.
FT      REPEAT          341          378           WD 2.
FT      REPEAT          381          418           WD 3.
FT      REPEAT          424          461           WD 4.
FT      REPEAT          464          503           WD 5.
FT      REPEAT          505          541           WD 6.
FT      REPEAT          553          590           WD 7.
FT      VARSPLIC        17           52           Missing (in isoform 2).
FT                                     /FTId=VSP_006764.
FT      VARIANT         543          543           A -> S (in dbSNP:4151060).
FT                                     /FTId=VAR_022027.
FT      VARIANT         592          592           P -> H (in dbSNP:2270439).
FT                                     /FTId=VAR_020119.
FT      STRAND          176          176
FT      HELIX           180          183
FT      TURN            184          184
FT      HELIX           185          187

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FT	TURN	188	188
FT	HELIX	190	197
FT	TURN	198	199
FT	HELIX	202	211
FT	HELIX	213	221
FT	TURN	222	223
FT	HELIX	224	233
FT	TURN	234	234
FT	STRAND	235	235
FT	HELIX	237	244
FT	STRAND	245	247
FT	HELIX	248	251
FT	STRAND	265	265
FT	HELIX	266	285
FT	TURN	286	288
FT	STRAND	296	297
FT	STRAND	301	302
FT	STRAND	306	310
FT	STRAND	313	323
FT	STRAND	325	332
FT	STRAND	335	339
FT	STRAND	343	344
FT	STRAND	346	350
FT	STRAND	353	360
FT	TURN	361	362
FT	STRAND	363	363
FT	STRAND	365	372
FT	STRAND	375	379
FT	STRAND	384	384
FT	STRAND	386	390
FT	TURN	393	394
FT	STRAND	395	400
FT	TURN	401	402
FT	STRAND	403	403

Alignment Scores:

Pred. No.:	0	Length:	605
Score:	3006.00	Matches:	569
Percent Similarity:	94.0%	Conservative:	0
Best Local Similarity:	94.0%	Mismatches:	0
Query Match:	77.9%	Indels:	36
DB:	1	Gaps:	1

HSBTRCP (1-2151) x FBW1A_HUMAN (1-605)

Qy	70	ATGGACCCGGCCGAGGCGGTGCTGCAAGAGAAGGCACTCAAGTTTATG-----	117
Db	1	MetAspProAlaGluAlaValLeuGlnGluLysAlaLeuLysPheMetCysSerMetPro	20
Qy	117	-----	117
Db	21	ArgSerLeuTrpLeuGlyCysSerSerLeuAlaAspSerMetProSerLeuArgCysLeu	40
Qy	118	-----AATTCCTCAGAGAGAGAAGACTGT	141
Db	41	TyrAsnProGlyThrGlyAlaLeuThrAlaPheGlnAsnSerSerGluArgGluAspCys	60

Qy	142	AATAATGGCGAACCCCTAGGAAGATAATACCAGAGAAGAATTCACCTTAGACAGACATAC	201
Db	61	AsnAsnGlyGluProProArgLysIleIleProGluLysAsnSerLeuArgGlnThrTyr	80
Qy	202	AACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGTATGTTTAGCAAGCACTGCTATG	261
Db	81	AsnSerCysAlaArgLeuCysLeuAsnGlnGluThrValCysLeuAlaSerThrAlaMet	100
Qy	262	AAGACTGAGAATTGTGTGGCCAAAACAAAACCTTGCCAATGGCACTTCCAGTATGATTGTG	321
Db	101	LysThrGluAsnCysValAlaLysThrLysLeuAlaAsnGlyThrSerSerMetIleVal	120
Qy	322	CCCAAGCAACGGAAACTCTCAGCAAGCTATGAAAAGGAAAAGGAACGTGTGTGTCAAATAC	381
Db	121	ProLysGlnArgLysLeuSerAlaSerTyrGluLysGluLysGluLeuCysValLysTyr	140
Qy	382	TTTGAGCAGTGGTCAGAGTCAGATCAAGTGGAATTTGTGGAACATCTTATATCCCAAATG	441
Db	141	PheGluGlnTrpSerGluSerAspGlnValGluPheValGluHisLeuIleSerGlnMet	160
Qy	442	TGTCATTACCAACATGGGCACATAAACTCGTATCTTAAACCTATGTTGCAGAGAGATTTTC	501
Db	161	CysHisTyrGlnHisGlyHisIleAsnSerTyrLeuLysProMetLeuGlnArgAspPhe	180
Qy	502	ATAACTGCTCTGCCAGCTCGGGGATTGGATCATATCGCTGAGAACATTCTGTCATACCTG	561
Db	181	IleThrAlaLeuProAlaArgGlyLeuAspHisIleAlaGluAsnIleLeuSerTyrLeu	200
Qy	562	GATGCCAAATCACTATGTGCTGCTGAACTTGTGTGCAAGGAATGGTACCGAGTGACCTCT	621
Db	201	AspAlaLysSerLeuCysAlaAlaGluLeuValCysLysGluTrpTyrArgValThrSer	220
Qy	622	GATGGCATGCTGTGGAAGAAGCTTATCGAGAGAATGGTCAGGACAGATTCTCTGTGGAGA	681
Db	221	AspGlyMetLeuTrpLysLysLeuIleGluArgMetValArgThrAspSerLeuTrpArg	240
Qy	682	GGCCTGGCAGAACGAAGAGGATGGGGACAGTATTTATTCAAAAACAAACCTCCTGACGGG	741
Db	241	GlyLeuAlaGluArgArgGlyTrpGlyGlnTyrLeuPheLysAsnLysProProAspGly	260
Qy	742	AATGCTCCTCCCAACTCTTTTTATAGAGCACTTTATCCTAAAATTATACAAGACATTGAG	801
Db	261	AsnAlaProProAsnSerPheTyrArgAlaLeuTyrProLysIleIleGlnAspIleGlu	280
Qy	802	ACAATAGAATCTAATTGGAGATGTGGAAGACATAGTTTACAGAGAATTCACCTGCCGAAGT	861
Db	281	ThrIleGluSerAsnTrpArgCysGlyArgHisSerLeuGlnArgIleHisCysArgSer	300
Qy	862	GAAACAAGCAAAGGAGTTTACTGTTTACAGTATGATGATCAGAAAATAGTAAGCGGCCTT	921
Db	301	GluThrSerLysGlyValTyrCysLeuGlnTyrAspAspGlnLysIleValSerGlyLeu	320
Qy	922	CGAGACAACACAATCAAGATCTGGGATAAAAAACACATTGGAATGCAAGCGAATTCTCACA	981
Db	321	ArgAspAsnThrIleLysIleTrpAspLysAsnThrLeuGluCysLysArgIleLeuThr	340
Qy	982	GGCCATACAGGTTCAGTCCTCTGTCTCCAGTATGATGAGAGAGTGATCATAACAGGATCA	1041

Db	341	 GlyHisThrGlySerValLeuCysLeuGlnTyrAspGluArgValIleIleThrGlySer	360
Qy	1042	TCGGATTCCACGGTCAGAGTGTGGGATGTAAATACAGGTGAAATGCTAAACACGTTGATT	1101
Db	361	 SerAspSerThrValArgValTrpAspValAsnThrGlyGluMetLeuAsnThrLeuIle	380
Qy	1102	CACCATTTGTGAAGCAGTTCTGCACTTGCCTTTCAATAATGGCATGATGGTGACCTGCTCC	1161
Db	381	 HisHisCysGluAlaValLeuHisLeuArgPheAsnAsnGlyMetMetValThrCysSer	400
Qy	1162	AAAGATCGTTCCATTGCTGTATGGGATATGGCCTCCCCAACTGACATTACCTCCGGAGG	1221
Db	401	 LysAspArgSerIleAlaValTrpAspMetAlaSerProThrAspIleThrLeuArgArg	420
Qy	1222	GTGCTGGTCGGACACCGAGCTGCTGTCAATGTTGTAGACTTTGATGACAAGTACATTGTT	1281
Db	421	 ValLeuValGlyHisArgAlaAlaValAsnValValAspPheAspAspLysTyrIleVal	440
Qy	1282	TCTGCATCTGGGGATAGAACTATAAAGGTATGGAACACAAGTACTTGTGAATTTGTAAGG	1341
Db	441	 SerAlaSerGlyAspArgThrIleLysValTrpAsnThrSerThrCysGluPheValArg	460
Qy	1342	ACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGCAGTACAGGGACAGGCTGGTAGTG	1401
Db	461	 ThrLeuAsnGlyHisLysArgGlyIleAlaCysLeuGlnTyrArgAspArgLeuValVal	480
Qy	1402	AGTGGCTCATCTGACAACACTATCAGATTATGGGACATAGAATGTGGTGCATGTTTACGA	1461
Db	481	 SerGlySerSerAspAsnThrIleArgLeuTrpAspIleGluCysGlyAlaCysLeuArg	500
Qy	1462	GTGTTAGAAGGCCATGAGGAATTGGTGCCTTGTATTTCGATTTGATAACAAGAGGATAGTC	1521
Db	501	 ValLeuGluGlyHisGluGluLeuValArgCysIleArgPheAspAsnLysArgIleVal	520
Qy	1522	AGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGATCTTGTGGCTGCTTTGGACCCCCGT	1581
Db	521	 SerGlyAlaTyrAspGlyLysIleLysValTrpAspLeuValAlaAlaLeuAspProArg	540
Qy	1582	GCTCCTGCAGGGACACTCTGTCTACGGACCTTGTGGAGCATTCGGGAAGAGTTTTTCGA	1641
Db	541	 AlaProAlaGlyThrLeuCysLeuArgThrLeuValGluHisSerGlyArgValPheArg	560
Qy	1642	CTACAGTTTGATGAATTCCAGATTGTCAGTAGTTCACATGATGACACAATCCTCATCTGG	1701
Db	561	 LeuGlnPheAspGluPheGlnIleValSerSerSerHisAspAspThrIleLeuIleTrp	580
Qy	1702	GACTTCCTAAATGATCCAGCTGCCCAAGCTGAACCCCCCGTTCCCTTCTCGAACATAC	1761
Db	581	 AspPheLeuAsnAspProAlaAlaGlnAlaGluProProArgSerProSerArgThrTyr	600
Qy	1762	ACCTACATCTCCAGA	1776
Db	601	 ThrTyrIleSerArg	605

RESULT 2
FBW1A_HUMAN

ID FBW1A_HUMAN STANDARD; PRT; 605 AA.
 AC Q9Y297; Q9Y213;
 DT 21-FEB-2001, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1999, sequence version 1.
 DT 07-FEB-2006, entry version 52.
 DE F-box/WD-repeat protein 1A (F-box and WD-repeats protein beta-TrCP)
 DE (E3RSIkappaB) (pIkappaBalph-E3 receptor subunit).
 GN Name=BTRC; Synonyms=BTRCP, FBW1A, FBXW1A;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
 RX MEDLINE=99075339; PubMed=9859996; DOI=10.1038/25159;
 RA Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
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 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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 RC TISSUE=B-cell;
 RX MEDLINE=20437281; PubMed=10983987; DOI=10.1016/S1097-2765(00)00040-X;
 RA Kleijnen M.F., Shih A.H., Zhou P., Kumar S., Soccio R.E.,
 RA Kedersha N.L., Gill G., Howley P.M.;
 RT "The hPLIC proteins may provide a link between the ubiquitination
 RT machinery and the proteasome.";
 RL Mol. Cell 6:409-419(2000).
 RN [7]
 RP INTERACTION WITH PHOSPHORYLATED CTNNB1.
 RX MEDLINE=22072105; PubMed=12077367;
 RA Sadot E., Conacci-Sorrell M., Zhurinsky J., Shnizer D., Lando Z.,
 RA Zharhary D., Kam Z., Ben-Ze'ev A., Geiger B.;
 RT "Regulation of S33/S37 phosphorylated beta-catenin in normal and
 RT transformed cells.";
 RL J. Cell Sci. 115:2771-2780(2002).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.95 ANGSTROMS) OF 175-605 IN COMPLEX WITH SKP1
 RP AND CTNNB1.
 RX MEDLINE=22706071; PubMed=12820959; DOI=10.1016/S1097-2765(03)00234-X;
 RA Wu G., Xu G., Schulman B.A., Jeffrey P.D., Harper J.W.,
 RA Pavletich N.P.;
 RT "Structure of a beta-TrCP1-Skp1-beta-catenin complex: destruction
 RT motif binding and lysine specificity of the SCF(beta-TrCP1) ubiquitin
 RT ligase.";
 RL Mol. Cell 11:1445-1456(2003).
 CC -!- FUNCTION: Substrate-recognition component of the SCF (SKP1-CUL1-F-
 CC box protein) ubiquitin ligase complex, which mediates the
 CC ubiquitination of proteins involved in cell cycle progression,
 CC signal transduction and transcription. Regulates the stability of
 CC CTNNB1 and participates in Wnt signaling.
 CC -!- PATHWAY: Ubiquitin conjugation; third step.
 CC -!- SUBUNIT: Interacts directly with SKP1 in the SCF complex.
 CC Interacts specifically with phosphorylated CTNNB1 and NFKBIA,
 CC ubiquitination substrates. Binds UBQLN1.
 CC -!- SUBCELLULAR LOCATION: Cytoplasm.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9Y297-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9Y297-2; Sequence=VSP_006764;
 CC -!- SIMILARITY: Contains 1 F-box domain.

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CC      -!- SIMILARITY: Contains 7 WD repeats.
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CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AF101784; AAD08702.1; -; mRNA.
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DR      Ensembl; ENSG00000166167; Homo sapiens.
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DR      LinkHub; Q9Y297; -.
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DR      GO; GO:0007165; P:signal transduction; TAS.
DR      GO; GO:0006511; P:ubiquitin-dependent protein catabolism; TAS.
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DR      ProDom; PD000018; WD40; 4.
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DR      SMART; SM00320; WD40; 7.
DR      PROSITE; PS50181; FBOX; 1.
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KW      Ub1 conjugation pathway; WD repeat; Wnt signaling pathway.
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FT      TURN            198       199
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FT      HELIX           213       221

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FT	STRAND	343	344
FT	STRAND	346	350
FT	STRAND	353	360
FT	TURN	361	362
FT	STRAND	363	363
FT	STRAND	365	372
FT	STRAND	375	379
FT	STRAND	384	384
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FT	TURN	393	394
FT	STRAND	395	400
FT	TURN	401	402
FT	STRAND	403	403

Alignment Scores:

Pred. No.:	0	Length:	605
Score:	3006.00	Matches:	569
Percent Similarity:	94.0%	Conservative:	0
Best Local Similarity:	94.0%	Mismatches:	0
Query Match:	77.9%	Indels:	36
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HSBTRCP (1-2151) x FBW1A_HUMAN (1-605)

Qy	70	ATGGACCCGGCCGAGGCGGTGCTGCAAGAGAAGGCACTCAAGTTTATG-----	117
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Qy	117	-----	117
Db	21	ArgSerLeuTrpLeuGlyCysSerSerLeuAlaAspSerMetProSerLeuArgCysLeu	40
Qy	118	-----AATTCCTCAGAGAGAGAAGACTGT	141
Db	41	TyrAsnProGlyThrGlyAlaLeuThrAlaPheGlnAsnSerSerGluArgGluAspCys	60
Qy	142	AATAATGGCGAACCCCTAGGAAGATAATACCAGAGAAGAATTCACCTAGACAGACATAC	201
Db	61	AsnAsnGlyGluProProArgLysIleIleProGluLysAsnSerLeuArgGlnThrTyr	80
Qy	202	AACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGTATGTTTAGCAAGCACTGCTATG	261

Db	81		AsnSerCysAlaArgLeuCysLeuAsnGlnGluThrValCysLeuAlaSerThrAlaMet	100
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Db	101		LysThrGluAsnCysValAlaLysThrLysLeuAlaAsnGlyThrSerSerMetIleVal	120
Qy	322	CCCAAGCAACGGAACTCTCAGCAAGCTATGAAAAGGAAAAGGAACTGTGTGTCAAATAC	381	
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Qy	382	TTTGAGCAGTGGTCAGAGTCAGATCAAGTGGAAATTTGTGGAACATCTTATATCCCAAATG	441	
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Qy	442	TGTCATTACCAACATGGGCACATAAACTCGTATCTTAAACCTATGTTGCAGAGAGATTTTC	501	
Db	161		CysHisTyrGlnHisGlyHisIleAsnSerTyrLeuLysProMetLeuGlnArgAspPhe	180
Qy	502	ATAACTGCTCTGCCAGCTCGGGGATTGGATCATATCGCTGAGAACATTCTGTCATACCTG	561	
Db	181		IleThrAlaLeuProAlaArgGlyLeuAspHisIleAlaGluAsnIleLeuSerTyrLeu	200
Qy	562	GATGCCAAATCACTATGTGCTGCTGAACTTGTGTGCAAGGAATGGTACCGAGTGACCTCT	621	
Db	201		AspAlaLysSerLeuCysAlaAlaGluLeuValCysLysGluTrpTyrArgValThrSer	220
Qy	622	GATGGCATGCTGTGGAAGAAGCTTATCGAGAGAATGGTCAGGACAGATTCTCTGTGGAGA	681	
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Qy	682	GGCCTGGCAGAACGAAGAGGATGGGGACAGTATTTATTCAAAAACAAACCTCCTGACGGG	741	
Db	241		GlyLeuAlaGluArgArgGlyTrpGlyGlnTyrLeuPheLysAsnLysProProAspGly	260
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Db	261		AsnAlaProProAsnSerPheTyrArgAlaLeuTyrProLysIleIleGlnAspIleGlu	280
Qy	802	ACAATAGAATCTAATTGGAGATGTGGAAGACATAGTTTACAGAGAATTCCTGCCGAAGT	861	
Db	281		ThrIleGluSerAsnTrpArgCysGlyArgHisSerLeuGlnArgIleHisCysArgSer	300
Qy	862	GAAACAAGCAAAGGAGTTTACTGTTTACAGTATGATGATCAGAAAATAGTAAGCGGCCTT	921	
Db	301		GluThrSerLysGlyValTyrCysLeuGlnTyrAspAspGlnLysIleValSerGlyLeu	320
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Qy	982	GGCCATACAGGTTTCAGTCCTCTGTCTCCAGTATGATGAGAGAGTGATCATAACAGGATCA	1041	
Db	341		GlyHisThrGlySerValLeuCysLeuGlnTyrAspGluArgValIleIleThrGlySer	360
Qy	1042	TCGGATTCCACGGTCAGAGTGTGGGATGTAAATACAGGTGAAATGCTAAACACGTTGATT	1101	

Db	361	SerAspSerThrValArgValTrpAspValAsnThrGlyGluMetLeuAsnThrLeuIle	380
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Db	381	HisHisCysGluAlaValLeuHisLeuArgPheAsnAsnGlyMetMetValThrCysSer	400
Qy	1162	AAAGATCGTTCCATTGCTGTATGGGATATGGCCTCCCCAACTGACATTACCCTCCGGAGG	1221
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Qy	1282	TCTGCATCTGGGGATAGAACTATAAAGGTATGGAACACAAGTACTTGTGAATTTGTAAGG	1341
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Qy	1342	ACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGCAGTACAGGGACAGGCTGGTAGTG	1401
Db	461	ThrLeuAsnGlyHisLysArgGlyIleAlaCysLeuGlnTyrArgAspArgLeuValVal	480
Qy	1402	AGTGGCTCATCTGACAACACTATCAGATTATGGGACATAGAATGTGGTGCATGTTTACGA	1461
Db	481	SerGlySerSerAspAsnThrIleArgLeuTrpAspIleGluCysGlyAlaCysLeuArg	500
Qy	1462	GTGTTAGAAGGCCATGAGGAATTGGTGCCTTGTATTTCGATTTGATAACAAGAGGATAGTC	1521
Db	501	ValLeuGluGlyHisGluGluLeuValArgCysIleArgPheAspAsnLysArgIleVal	520
Qy	1522	AGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGATCTTGTGGCTGCTTTGGACCCCCGT	1581
Db	521	SerGlyAlaTyrAspGlyLysIleLysValTrpAspLeuValAlaAlaLeuAspProArg	540
Qy	1582	GCTCCTGCAGGGACACTCTGTCTACGGACCTTGTGGAGCATTCCGGAAGAGTTTTTCGA	1641
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Db	581	AspPheLeuAsnAspProAlaAlaGlnAlaGluProProArgSerProSerArgThrTyr	600
Qy	1762	ACCTACATCTCCAGA	1776
Db	601	ThrTyrIleSerArg	605

RESULT 3

FBW1A_HUMAN

ID FBW1A_HUMAN STANDARD; PRT; 605 AA.

AC Q9Y297; Q9Y213;

DT 21-FEB-2001, integrated into UniProtKB/Swiss-Prot.

DT 01-NOV-1999, sequence version 1.

DT 07-FEB-2006, entry version 52.

DE F-box/WD-repeat protein 1A (F-box and WD-repeats protein beta-TrCP)
 DE (E3RSIkappaB) (pIkappaBalpha-E3 receptor subunit).
 GN Name=BTRC; Synonyms=BTRCP, FBW1A, FBXW1A;
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 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
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 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
 RX MEDLINE=99075339; PubMed=9859996; DOI=10.1038/25159;
 RA Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
 RA Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
 RT "Identification of the receptor component of the IkappaBalpha-
 RT ubiquitin ligase.";
 RL Nature 396:590-594(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
 RC TISSUE=Lymphoid;
 RX MEDLINE=98325370; PubMed=9660940; DOI=10.1016/S1097-2765(00)80056-8;
 RA Margottin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V.,
 RA Thomas D., Strebel K., Benarous R.;
 RT "A novel human WD protein, h-beta TrCp, that interacts with HIV-1 Vpu
 RT connects CD4 to the ER degradation pathway through an F-box motif.";
 RL Mol. Cell 1:565-574(1998).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
 RX MEDLINE=20003060; PubMed=10531035; DOI=10.1016/S0960-9822(00)80020-2;
 RA Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal M.,
 RA Pagano M.;
 RT "Identification of a family of human F-box proteins.";
 RL Curr. Biol. 9:1177-1179(1999).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]

RP CHARACTERIZATION.
RX MEDLINE=99145464; PubMed=9990852;
RA Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J.,
RA Harper J.W.;
RT "The SCF(beta-TRCP)-ubiquitin ligase complex associates specifically
RT with phosphorylated destruction motifs in I-kappa-B-alpha and beta-
RT catenin and stimulates I-kappa-B-alpha ubiquitination in vitro.";
RL Genes Dev. 13:270-283(1999).
RN [6]
RP INTERACTION WITH UBQLN1.
RC TISSUE=B-cell;
RX MEDLINE=20437281; PubMed=10983987; DOI=10.1016/S1097-2765(00)00040-X;
RA Kleijnen M.F., Shih A.H., Zhou P., Kumar S., Soccio R.E.,
RA Kedersha N.L., Gill G., Howley P.M.;
RT "The hPLIC proteins may provide a link between the ubiquitination
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RL Mol. Cell 6:409-419(2000).
RN [7]
RP INTERACTION WITH PHOSPHORYLATED CTNNB1.
RX MEDLINE=22072105; PubMed=12077367;
RA Sadot E., Conacci-Sorrell M., Zhurinsky J., Shnizer D., Lando Z.,
RA Zharhary D., Kam Z., Ben-Ze'ev A., Geiger B.;
RT "Regulation of S33/S37 phosphorylated beta-catenin in normal and
RT transformed cells.";
RL J. Cell Sci. 115:2771-2780(2002).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.95 ANGSTROMS) OF 175-605 IN COMPLEX WITH SKP1
RP AND CTNNB1.
RX MEDLINE=22706071; PubMed=12820959; DOI=10.1016/S1097-2765(03)00234-X;
RA Wu G., Xu G., Schulman B.A., Jeffrey P.D., Harper J.W.,
RA Pavletich N.P.;
RT "Structure of a beta-TrCP1-Skp1-beta-catenin complex: destruction
RT motif binding and lysine specificity of the SCF(beta-TrCP1) ubiquitin
RT ligase.";
RL Mol. Cell 11:1445-1456(2003).
CC -!- FUNCTION: Substrate-recognition component of the SCF (SKP1-CUL1-F-
CC box protein) ubiquitin ligase complex, which mediates the
CC ubiquitination of proteins involved in cell cycle progression,
CC signal transduction and transcription. Regulates the stability of
CC CTNNB1 and participates in Wnt signaling.
CC -!- PATHWAY: Ubiquitin conjugation; third step.
CC -!- SUBUNIT: Interacts directly with SKP1 in the SCF complex.
CC Interacts specifically with phosphorylated CTNNB1 and NFKBIA,
CC ubiquitination substrates. Binds UBQLN1.
CC -!- SUBCELLULAR LOCATION: Cytoplasm.
CC -!- ALTERNATIVE PRODUCTS:
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CC -!- SIMILARITY: Contains 1 F-box domain.
CC -!- SIMILARITY: Contains 7 WD repeats.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
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 DR MIM; 603482; gene.
 DR LinkHub; Q9Y297; -.
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 DR GO; GO:0007165; P:signal transduction; TAS.
 DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; TAS.
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 DR ProDom; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
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 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
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 KW Ubl conjugation pathway; WD repeat; Wnt signaling pathway.
 FT CHAIN 1 605 F-box/WD-repeat protein 1A.
 FT /FTId=PRO_0000050980.
 FT DOMAIN 190 228 F-box.
 FT REPEAT 301 338 WD 1.
 FT REPEAT 341 378 WD 2.
 FT REPEAT 381 418 WD 3.
 FT REPEAT 424 461 WD 4.
 FT REPEAT 464 503 WD 5.
 FT REPEAT 505 541 WD 6.
 FT REPEAT 553 590 WD 7.
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 FT /FTId=VAR_022027.
 FT VARIANT 592 592 P -> H (in dbSNP:2270439).
 FT /FTId=VAR_020119.
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 FT HELIX 180 183
 FT TURN 184 184
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 FT TURN 198 199
 FT HELIX 202 211
 FT HELIX 213 221
 FT TURN 222 223
 FT HELIX 224 233
 FT TURN 234 234
 FT STRAND 235 235
 FT HELIX 237 244

Qy	1238	CGGTGTCCGACCAGCACCCCTCCGGAGGGTAATGTCAGTTGGGGAGGCCATATCCCATACA	1179
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Db	287	ArgCysGlyArgHisSerLeuGlnArgIleHisCysArgSerGluThrSerLysGlyVal	306
Qy	1178	GCAATGGAACGATCTTTGGAGCAGGTCACCATCATGCCATTATTGAAACGCAAGTGCAGA	1119
		: : : : : : : : :	
Db	307	TyrCysLeuGlnTyrAspAspGlnLysIleValSerGlyLeu-----ArgAspAsn	323
Qy	1118	ACTGCTTCACAATGGTGAATCAACGTGTTTAGCATTTACCTGTATTTACATCCCACACT	1059
		: :	
Db	324	ThrIleLysIleTrpAspLysAsnThrLeuGluCysLysArgIleLeuThrGlyHisThr	343
Qy	1058	-----CTGACCGTGGAAATCCGATGATCCTGTTATGATCACTCTCTCATCATACTGG	1008
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Db	344	GlySerValLeuCysLeuGlnTyrAspGluArgValIleIleThrGlySerSer-----	361
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Qy	947	TCCCAGATCTTGATTGTGTTGTCTCGAAGG	918

Db 381 HisHisCysGluAlaValLeuHisLeuArg 390

RESULT 4

FBW1A_HUMAN

ID FBW1A_HUMAN STANDARD; PRT; 605 AA.
AC Q9Y297; Q9Y213;
DT 21-FEB-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 52.
DE F-box/WD-repeat protein 1A (F-box and WD-repeats protein beta-TrCP)
DE (E3RSIkappaB) (pIkappaBalpha-E3 receptor subunit).
GN Name=BTRC; Synonyms=BTRCP, FBW1A, FBXW1A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RX MEDLINE=99075339; PubMed=9859996; DOI=10.1038/25159;
RA Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
RA Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
RT "Identification of the receptor component of the IkappaBalpha-
RT ubiquitin ligase.";
RL Nature 396:590-594 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
RC TISSUE=Lymphoid;
RX MEDLINE=98325370; PubMed=9660940; DOI=10.1016/S1097-2765(00)80056-8;
RA Margottin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V.,
RA Thomas D., Strebel K., Benarous R.;
RT "A novel human WD protein, h-beta TrCp, that interacts with HIV-1 Vpu
RT connects CD4 to the ER degradation pathway through an F-box motif.";
RL Mol. Cell 1:565-574 (1998).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
RX MEDLINE=20003060; PubMed=10531035; DOI=10.1016/S0960-9822(00)80020-2;
RA Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal M.,
RA Pagano M.;
RT "Identification of a family of human F-box proteins.";
RL Curr. Biol. 9:1177-1179 (1999).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE=99145464; PubMed=9990852;
 RA Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J.,
 RA Harper J.W.;
 RT "The SCF(beta-TRCP)-ubiquitin ligase complex associates specifically
 RT with phosphorylated destruction motifs in I-kappa-B-alpha and beta-
 RT catenin and stimulates I-kappa-B-alpha ubiquitination in vitro.";
 RL Genes Dev. 13:270-283(1999).
 RN [6]
 RP INTERACTION WITH UBQLN1.
 RC TISSUE=B-cell;
 RX MEDLINE=20437281; PubMed=10983987; DOI=10.1016/S1097-2765(00)00040-X;
 RA Kleijnen M.F., Shih A.H., Zhou P., Kumar S., Soccio R.E.,
 RA Kedersha N.L., Gill G., Howley P.M.;
 RT "The hPLIC proteins may provide a link between the ubiquitination
 RT machinery and the proteasome.";
 RL Mol. Cell 6:409-419(2000).
 RN [7]
 RP INTERACTION WITH PHOSPHORYLATED CTNNB1.
 RX MEDLINE=22072105; PubMed=12077367;
 RA Sadot E., Conacci-Sorrell M., Zhurinsky J., Shnizer D., Lando Z.,
 RA Zharhary D., Kam Z., Ben-Ze'ev A., Geiger B.;
 RT "Regulation of S33/S37 phosphorylated beta-catenin in normal and
 RT transformed cells.";
 RL J. Cell Sci. 115:2771-2780(2002).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.95 ANGSTROMS) OF 175-605 IN COMPLEX WITH SKP1
 RP AND CTNNB1.
 RX MEDLINE=22706071; PubMed=12820959; DOI=10.1016/S1097-2765(03)00234-X;
 RA Wu G., Xu G., Schulman B.A., Jeffrey P.D., Harper J.W.,
 RA Pavletich N.P.;
 RT "Structure of a beta-TrCP1-Skp1-beta-catenin complex: destruction
 RT motif binding and lysine specificity of the SCF(beta-TrCP1) ubiquitin
 RT ligase.";
 RL Mol. Cell 11:1445-1456(2003).
 CC -!- FUNCTION: Substrate-recognition component of the SCF (SKP1-CUL1-F-
 CC box protein) ubiquitin ligase complex, which mediates the
 CC ubiquitination of proteins involved in cell cycle progression,
 CC signal transduction and transcription. Regulates the stability of
 CC CTNNB1 and participates in Wnt signaling.
 CC -!- PATHWAY: Ubiquitin conjugation; third step.
 CC -!- SUBUNIT: Interacts directly with SKP1 in the SCF complex.
 CC Interacts specifically with phosphorylated CTNNB1 and NFKBIA,
 CC ubiquitination substrates. Binds UBQLN1.
 CC -!- SUBCELLULAR LOCATION: Cytoplasm.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;

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CC      IsoId=Q9Y297-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q9Y297-2; Sequence=VSP_006764;
CC      -!- SIMILARITY: Contains 1 F-box domain.
CC      -!- SIMILARITY: Contains 7 WD repeats.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AF101784; AAD08702.1; -; mRNA.
DR      EMBL; Y14153; CAA74572.1; -; mRNA.
DR      EMBL; AF129530; AAF04464.1; -; mRNA.
DR      EMBL; BC027994; AAH27994.1; -; mRNA.
DR      PDB; 1P22; X-ray; A=175-605.
DR      IntAct; Q9Y297; -.
DR      Ensembl; ENSG00000166167; Homo sapiens.
DR      HGNC; HGNC:1144; BTRC.
DR      MIM; 603482; gene.
DR      LinkHub; Q9Y297; -.
DR      GO; GO:0004840; F:ubiquitin conjugating enzyme activity; TAS.
DR      GO; GO:0007165; P:signal transduction; TAS.
DR      GO; GO:0006511; P:ubiquitin-dependent protein catabolism; TAS.
DR      InterPro; IPR001810; F-box.
DR      InterPro; IPR001680; WD40.
DR      Pfam; PF00646; F-box; 1.
DR      Pfam; PF00400; WD40; 7.
DR      PRINTS; PR00320; GPROTEINBRPT.
DR      ProDom; PD000018; WD40; 4.
DR      SMART; SM00256; FBOX; 1.
DR      SMART; SM00320; WD40; 7.
DR      PROSITE; PS50181; FBOX; 1.
DR      PROSITE; PS00678; WD_REPEATS_1; 6.
DR      PROSITE; PS50082; WD_REPEATS_2; 7.
DR      PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW      3D-structure; Alternative splicing; Ligase; Polymorphism; Repeat;
KW      Ubl conjugation pathway; WD repeat; Wnt signaling pathway.
FT      CHAIN           1       605       F-box/WD-repeat protein 1A.
FT                                     /FTId=PRO_0000050980.
FT      DOMAIN          190       228       F-box.
FT      REPEAT          301       338       WD 1.
FT      REPEAT          341       378       WD 2.
FT      REPEAT          381       418       WD 3.
FT      REPEAT          424       461       WD 4.
FT      REPEAT          464       503       WD 5.
FT      REPEAT          505       541       WD 6.
FT      REPEAT          553       590       WD 7.
FT      VARSPLIC        17        52       Missing (in isoform 2).
FT                                     /FTId=VSP_006764.
FT      VARIANT         543       543       A -> S (in dbSNP:4151060).
FT                                     /FTId=VAR_022027.
FT      VARIANT         592       592       P -> H (in dbSNP:2270439).
FT                                     /FTId=VAR_020119.
FT      STRAND          176       176
FT      HELIX           180       183
FT      TURN            184       184
FT      HELIX           185       187
FT      TURN            188       188

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Alignment Scores:

Pred. No.:	0	Length:	605
Score:	57.50	Matches:	28
Percent Similarity:	37.3%	Conservative:	13
Best Local Similarity:	25.5%	Mismatches:	60
Query Match:	1.5%	Indels:	9
DB:	1	Gaps:	3

HSBTRCP (1-2151) x FBW1A HUMAN (1-605)

Qy	1238	CGGTGTCGCCAGCACCCTCCGGAGGGTAATGTCAGTTGGGGAGGCCATATCCCATAACA	1179
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Db	287	ArgCysGlyArgHisSerLeuGlnArgIleHisCysArgSerGluThrSerLysGlyVal	306
Qy	1178	GCAATGGAACGATCTTTGGAGCAGGTCACCATCATGCCATTATTGAAACGCAAGTGCAGA	1119
		: : : : : : : : : : :	
Db	307	TyrCysLeuGlnTyrAspAspGlnLysIleValSerGlyLeu-----ArgAspAsn	323
Qy	1118	ACTGCTTCACAATGGTGAATCAACGTGTTTAGCATTTACCTGTATTTACATCCCACACT	1059
		: : :	
Db	324	ThrIleLysIleTrpAspLysAsnThrLeuGluCysLysArgIleLeuThrGlyHisThr	343
Qy	1058	-----CTGACCGTGGAATCCGATGATCCTGTTATGATCACTCTCTCATCATACTGG	1008

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Db      344 GlySerValLeuCysLeuGlnTyrAspGluArgValIleIleThrGlySerSer----- 361
Qy      1007 AGACAGAGGACTGAACCTGTATGGCCTGTGAGAATTCGCTTGCATTCCAATGTGTTTTTA 948
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Db      362 ---AspSerThrValArgValTrpAspValAsnThrGlyGluMetLeuAsnThrLeuIle 380
Qy      947 TCCCAGATCTTGATTGTGTTGTCTCGAAGG 918
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Db      381 HisHisCysGluAlaValLeuHisLeuArg 390

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